

**Fig 1**

Consensus	$X_n$	-D-	$X_n$	-EE-	$X_n$	-DPiDgt-	$X_n$	-wd-	$X_{11}$	-GG-	$X_n$
	47		70		90		219		232		
Impase1	$X_{46}$	-D-	$X_{22}$	-EE-	$X_{18}$	-DPIDGT-	$X_{123}$	-WD-	$X_{11}$	-GG-	$X_{57}$
	54		79		153		315		328		
lptase	$X_{53}$	-D-	$X_{24}$	-EE-	$X_{72}$	-DPIDST-	$X_{156}$	-WD-	$X_{11}$	-GG-	$X_{70}$
	75		98		119		280		293		
Fbpase1	$X_{74}$	-D-	$X_{22}$	-EE-	$X_{19}$	-DPLDGS-	$X_{155}$	-YE-	$X_{11}$	-GG-	$X_{44}$

**Fig 2**

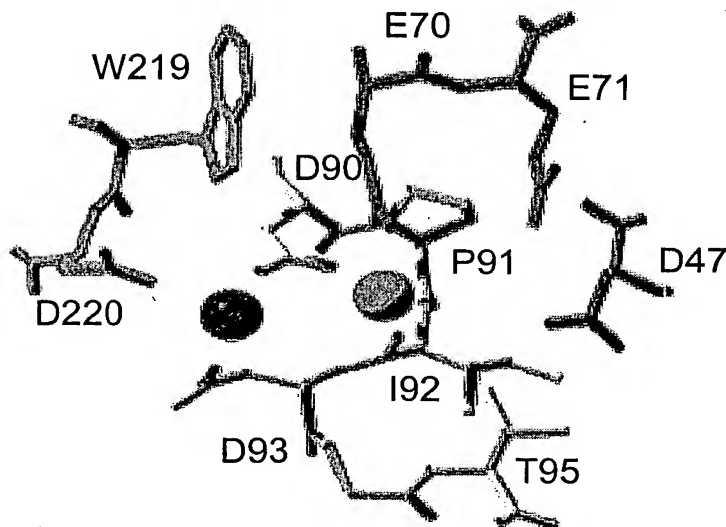


Fig 3

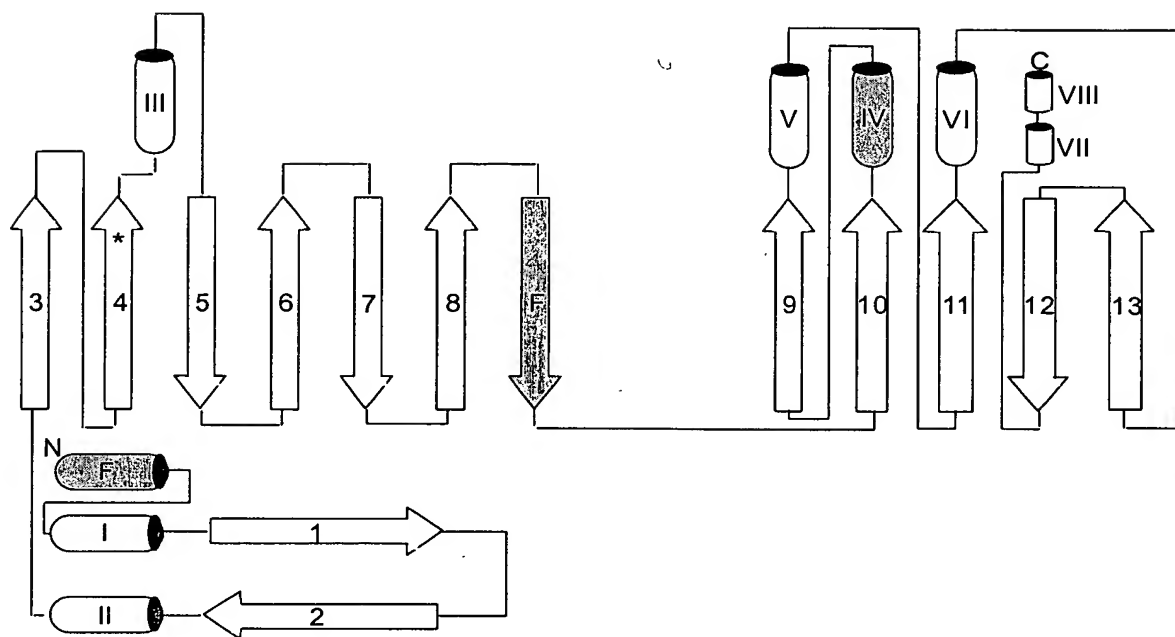
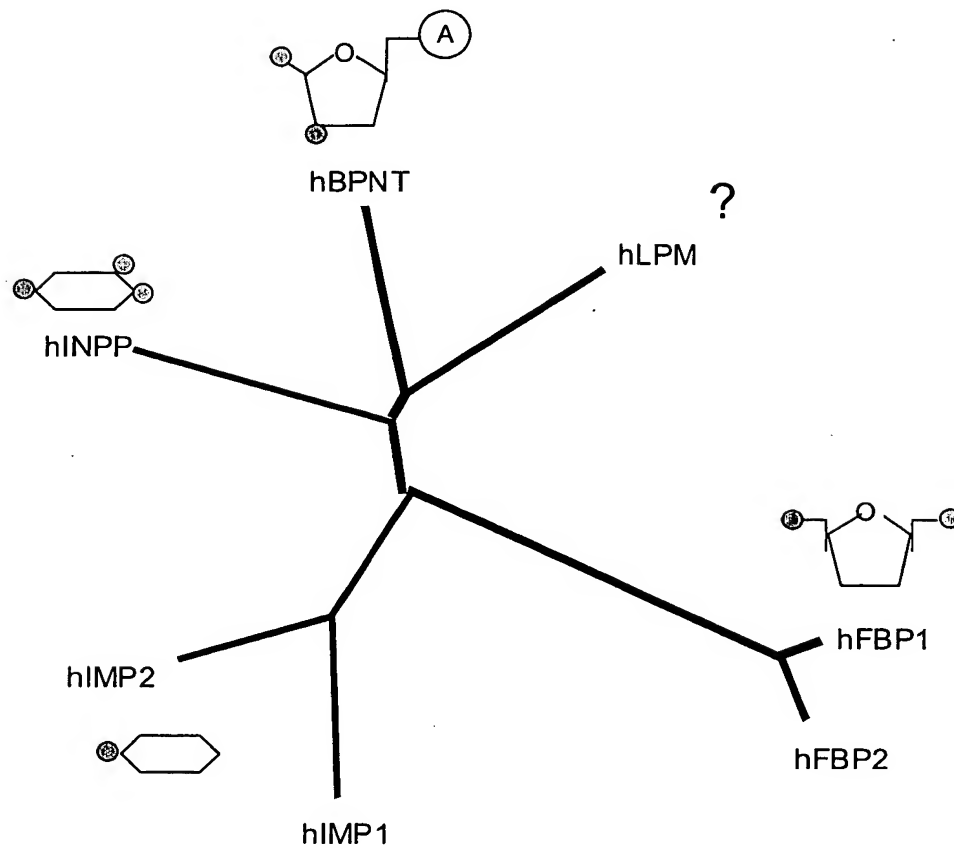


Fig 4



**Fig 5**

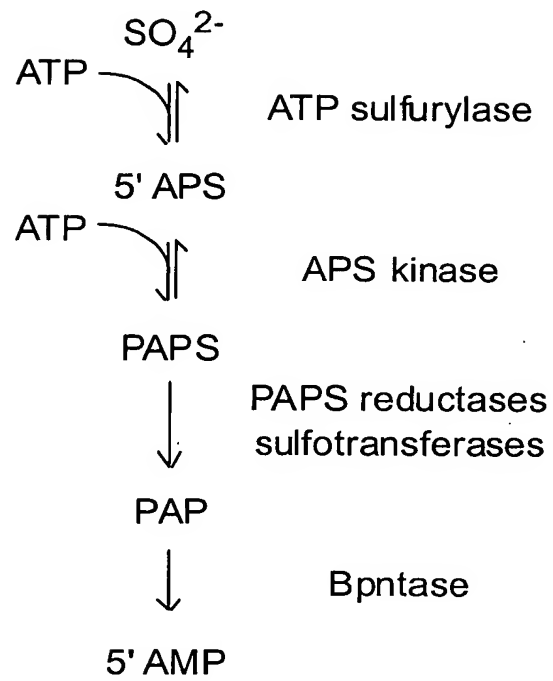


Fig 6

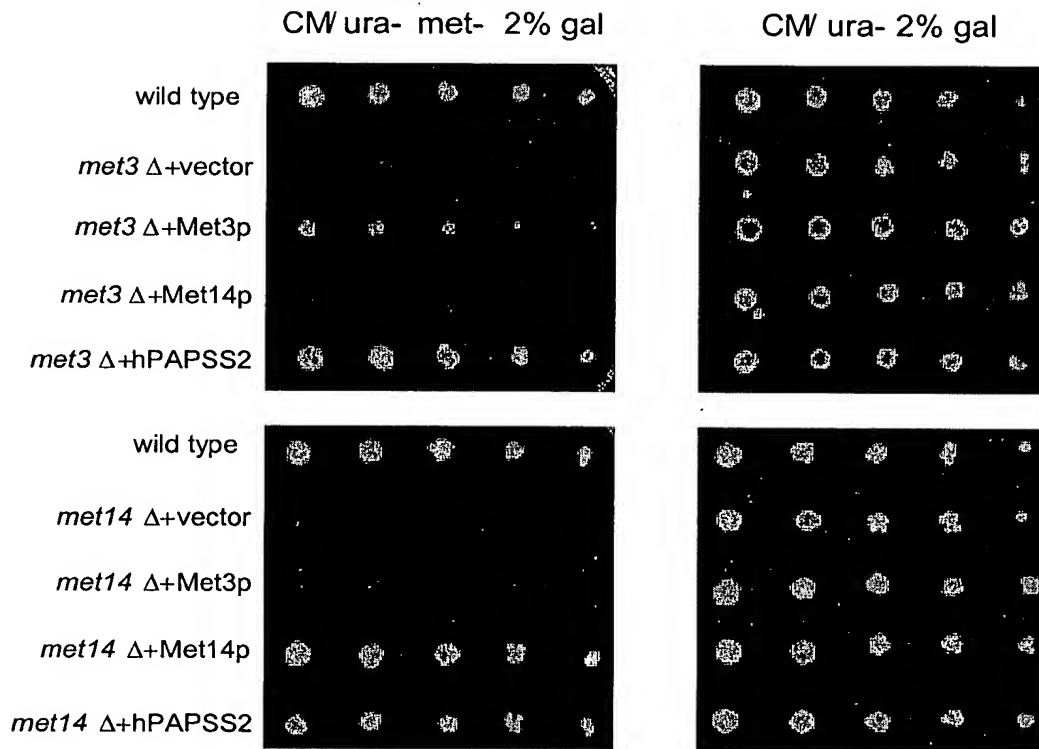


Fig 7

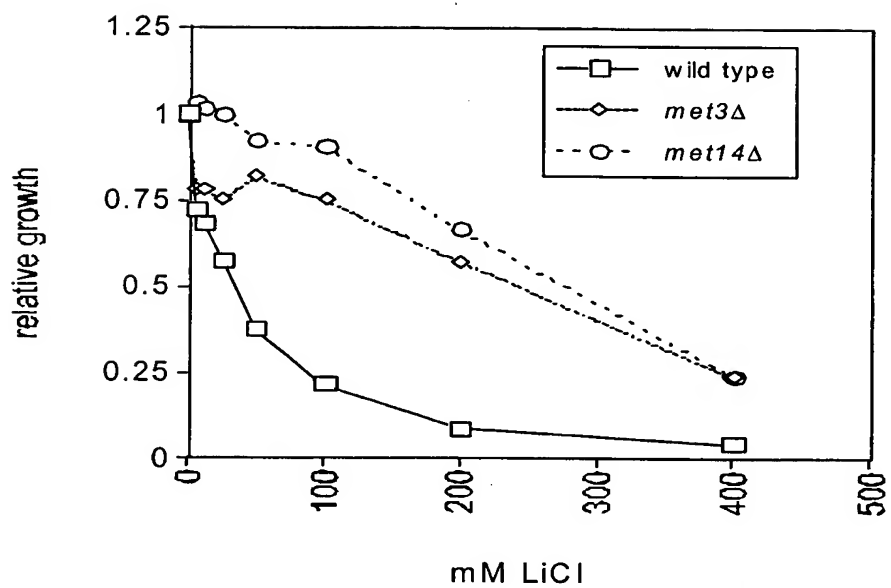


Fig 8

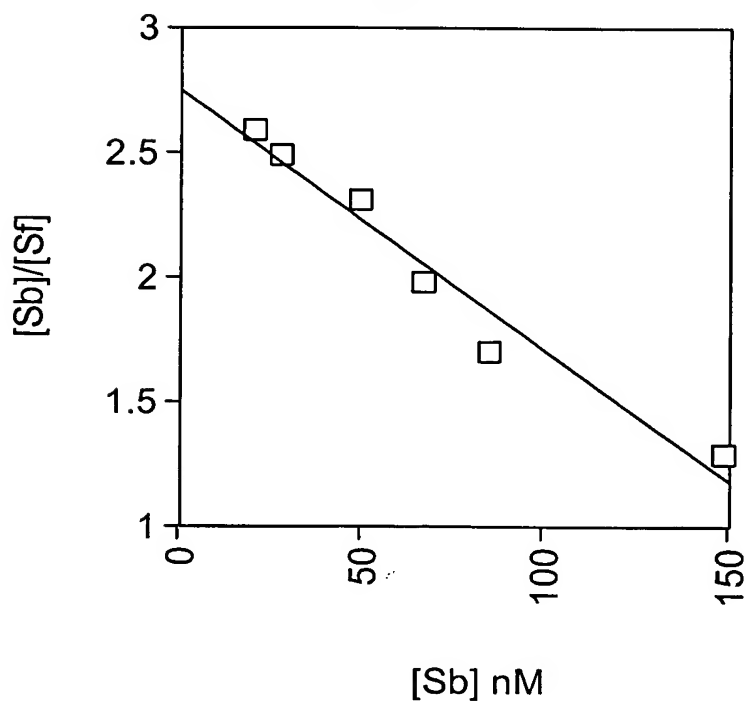


Fig 9

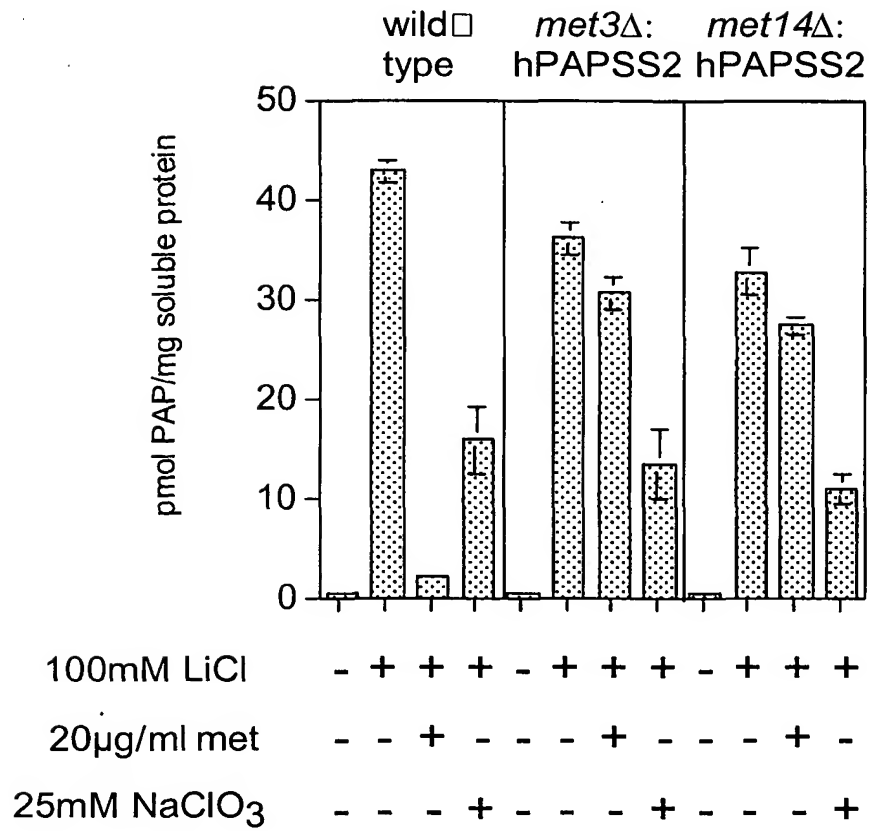
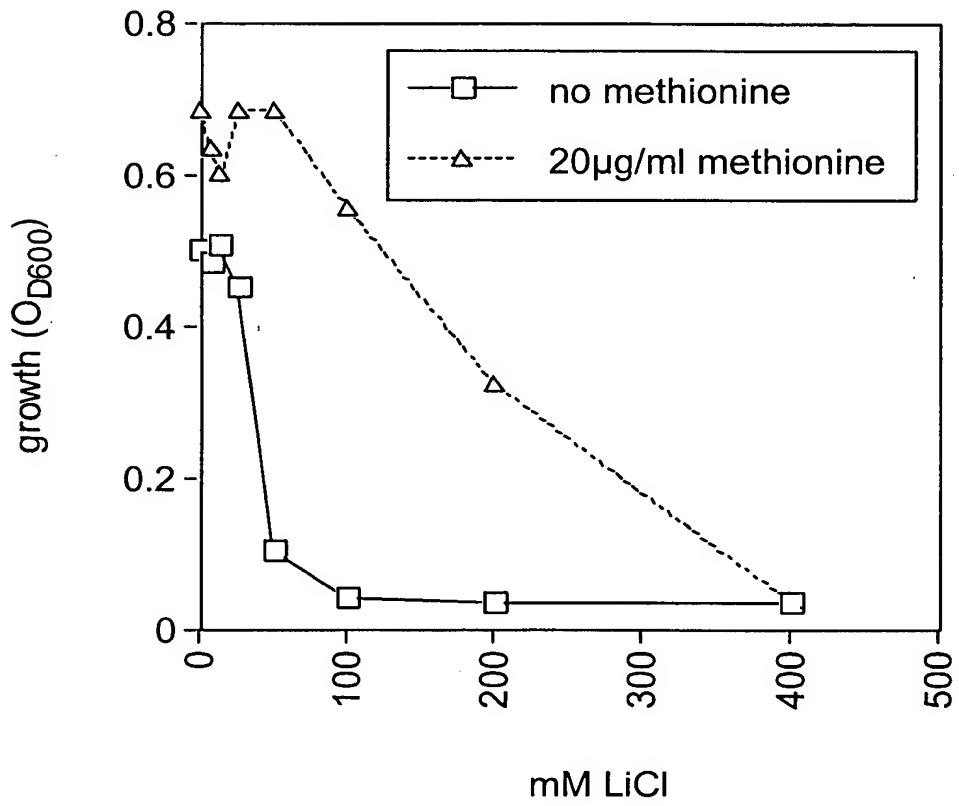
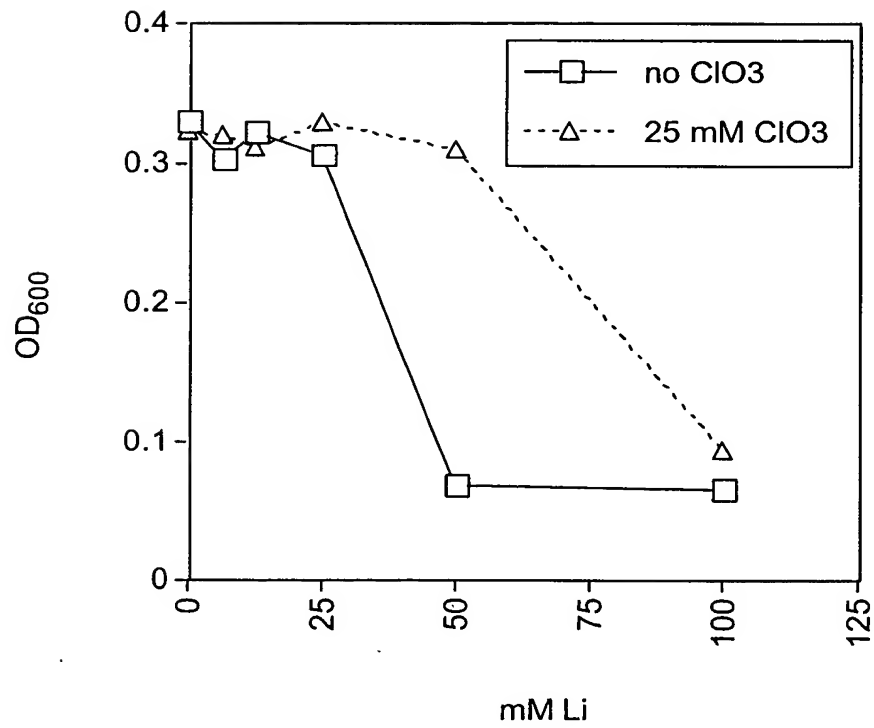


Fig 10





**Fig 11**



**Fig 12**

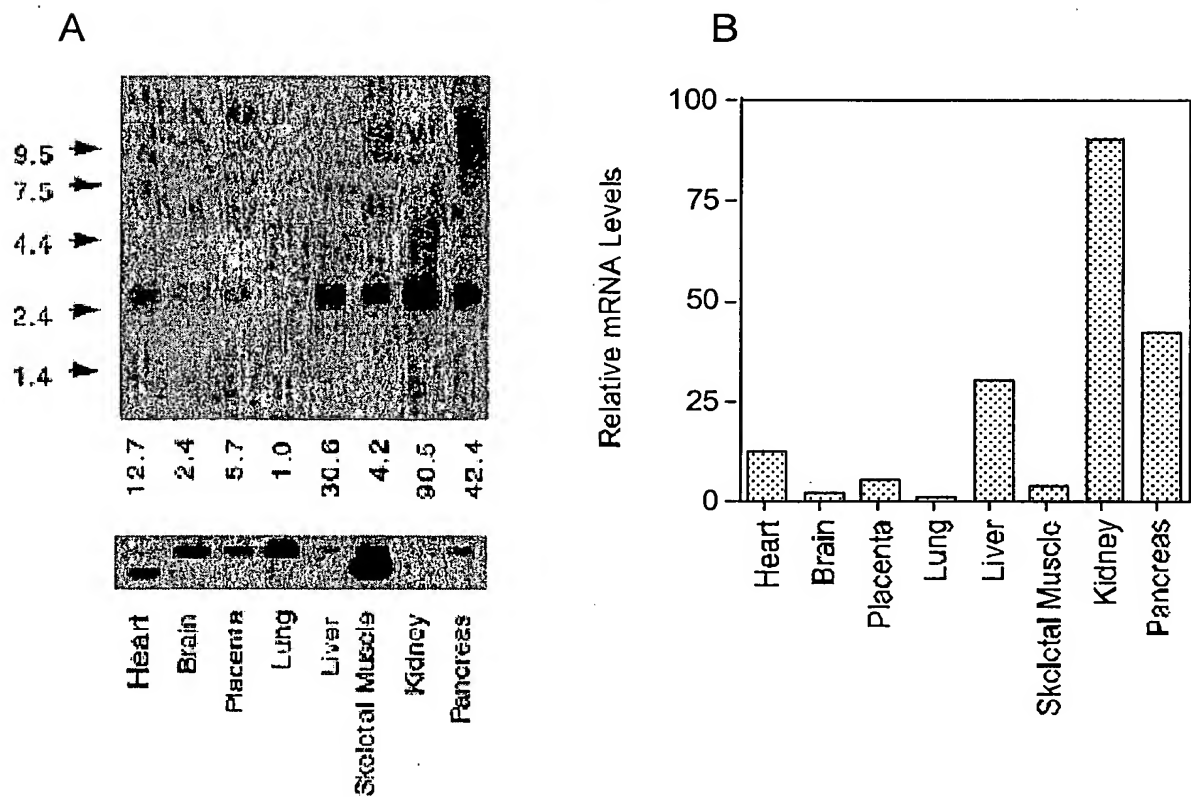


Fig 13

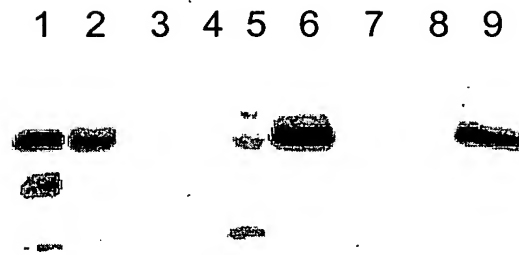
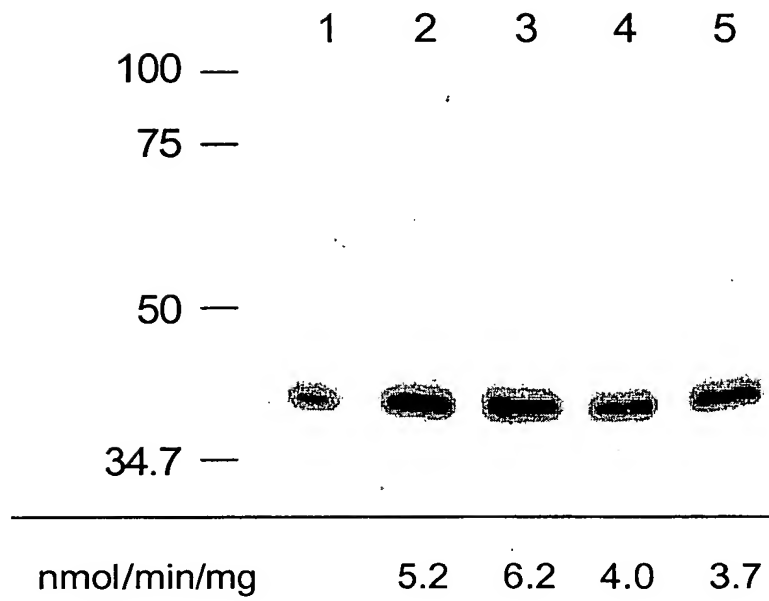


Fig 14



**Fig 15**

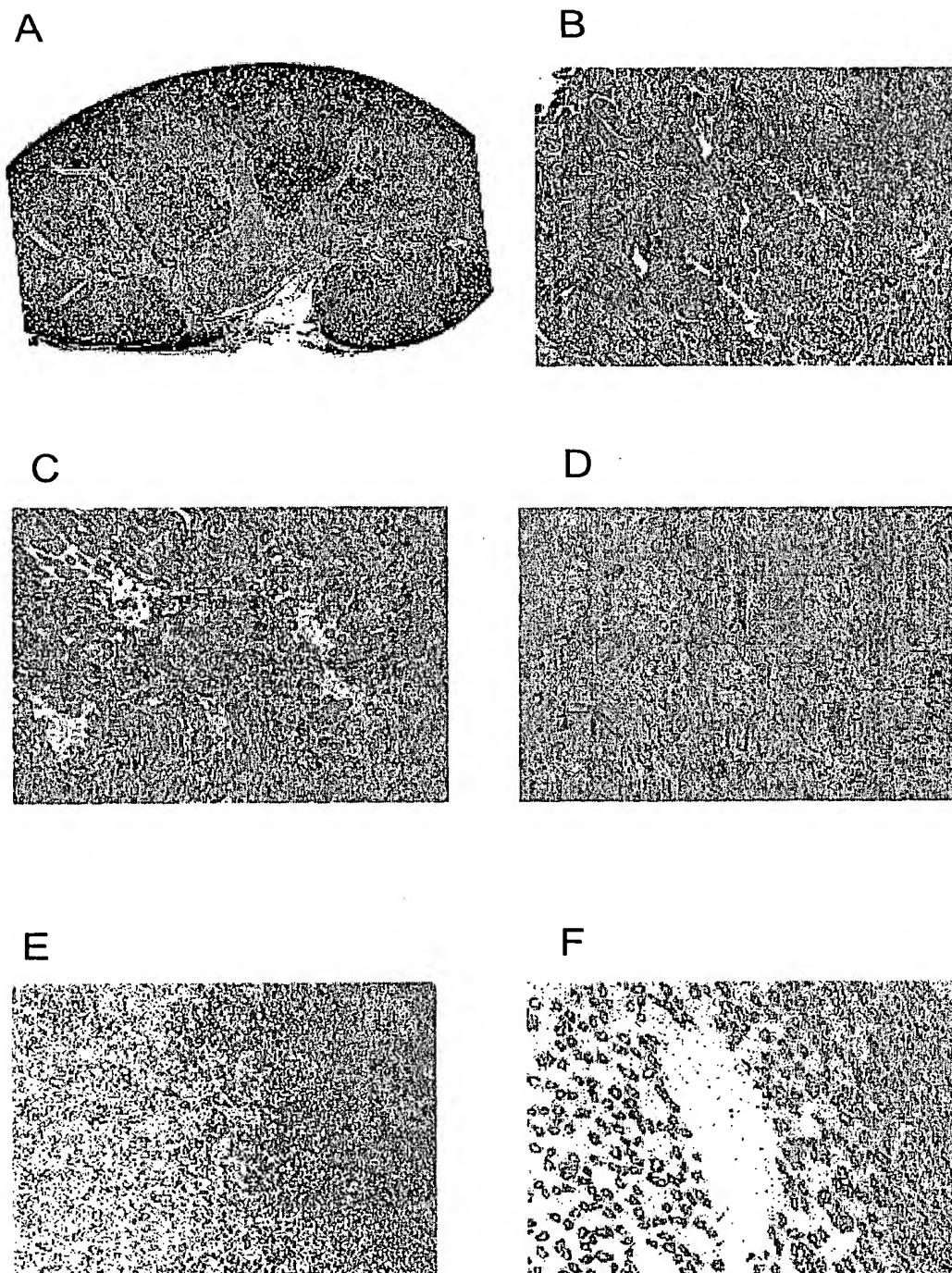
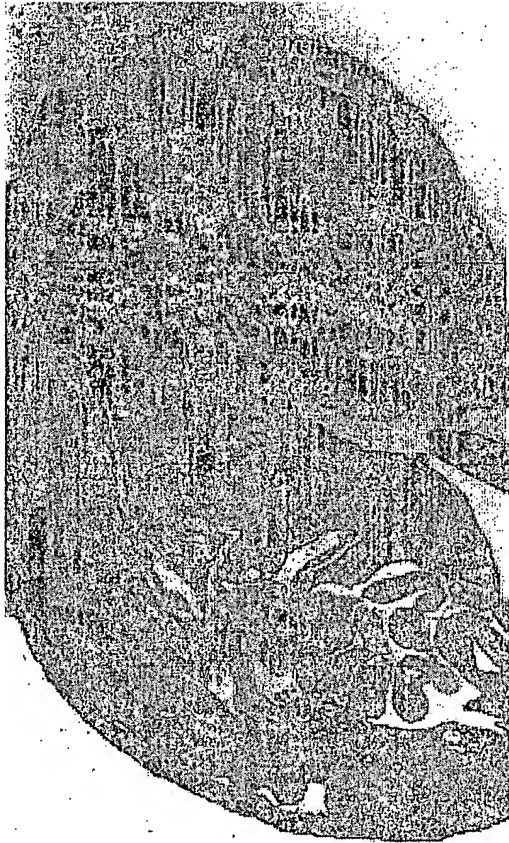


Fig 16

A



B



Fig 17

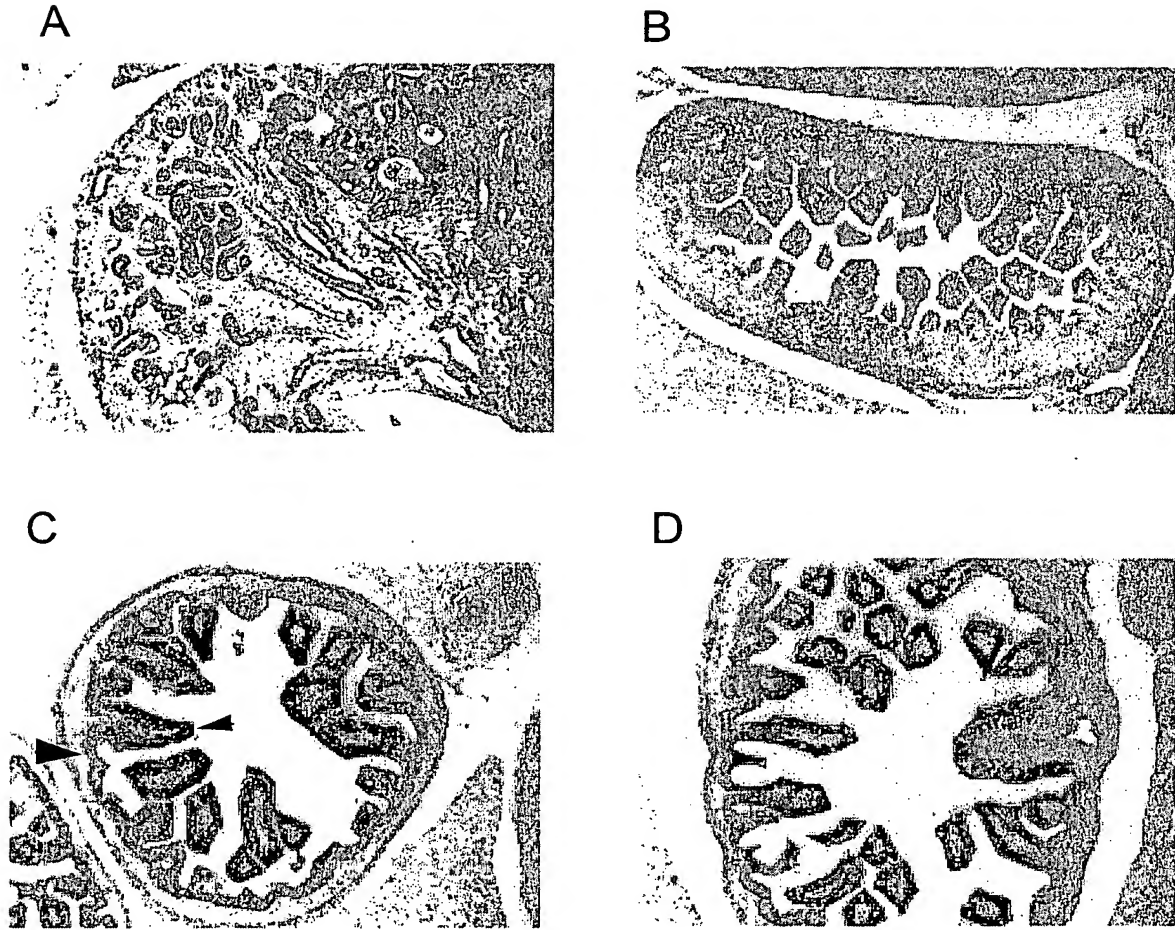


Fig 18

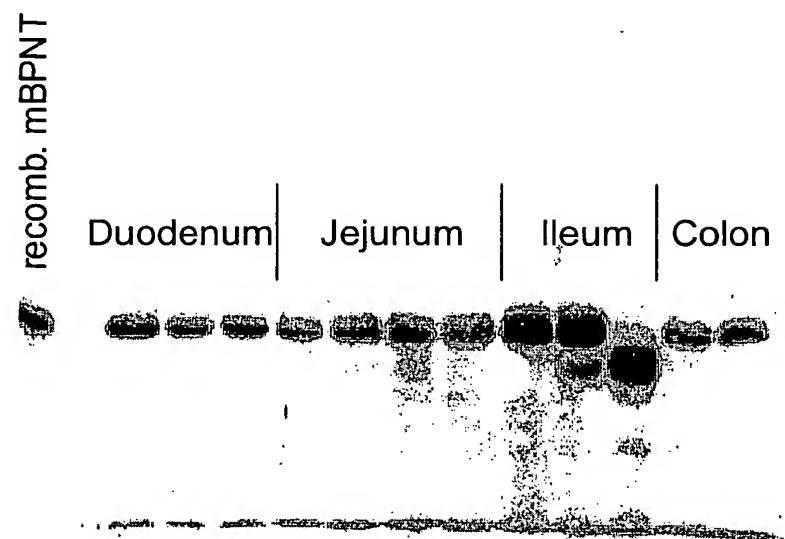


Fig 19

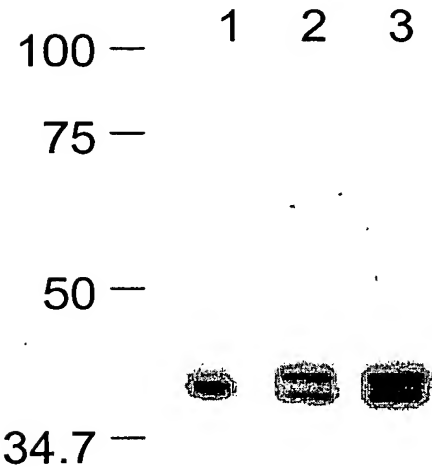
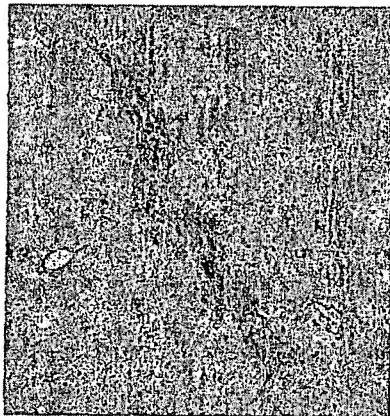


Fig 20

A



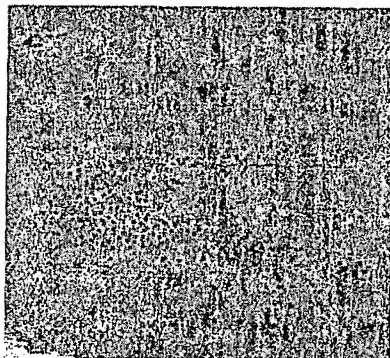
B



C



D



E

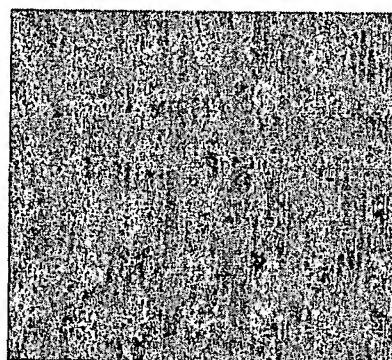


Fig 21

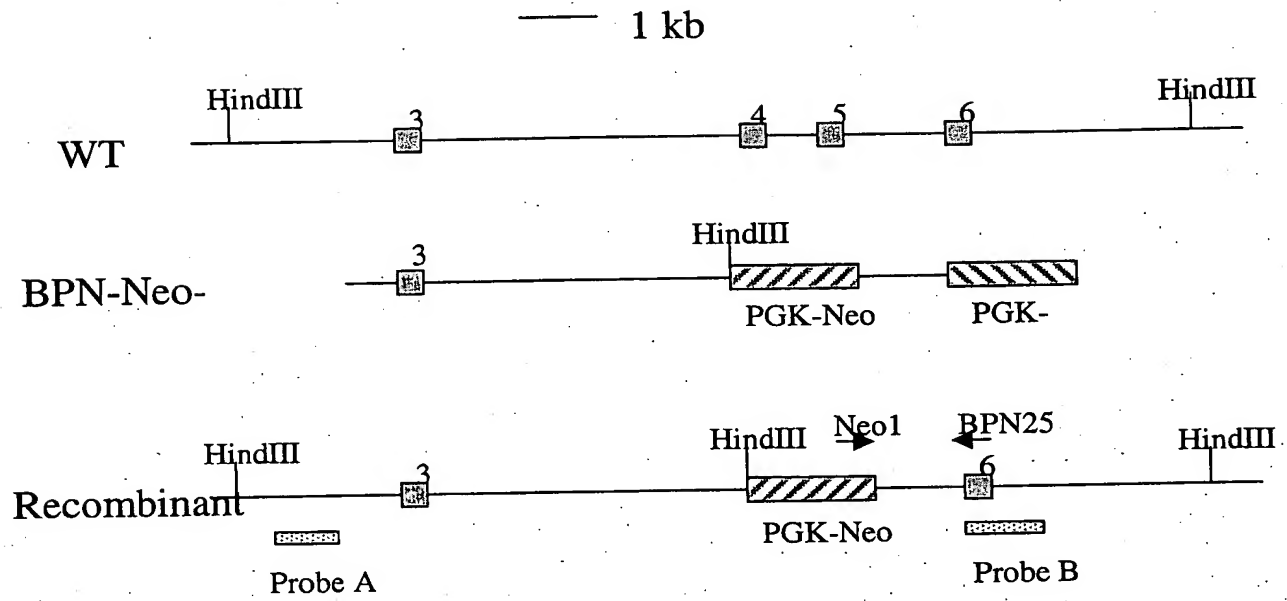




Fig 22A

	10	20	30	40	50	60	70	80	90	100
1	TGGCGAGCTT	GCTTATTCTG	CTTTCAGAGT	ATGGGGTGT	ATAAAGCAGC	TGGCGGCACA	CTGGGGTTTC	CCGACTCTTA	GCCCATTTAA	AGCAGGTTGG
101	AATCTAGAGC	GTTATGAAAG	AGTTTCTCAA	TTAGAGAAGA	GAATATTCCA	AATAATTAA	AAGCACCTTT	GCAAACTTGA	ACTGTTGTGG	AGCTGGGAAT
201	CGAGTTCAGT	GGTAGTGCCT	GCTTGGTGTG	TGTCAGGGGC	GTGTGTGATC	TCTATCAGCA	CACACACACA	CACACACACA	CACACACACA	CGCACACACA
301	CACGCACGCA	CACACACACG	CACACACGCA	CGCACACACG	CGCGCACACA	CACACACACA	CACACACACA	CACACACGCT	GTTTTAAACT	ATGATTGTTT
401	ATTGGTATAC	AGTTTTCACAC	GGTAGTACAA	GCTGATCTCA	GATTTCATGGC	TGTCCTTCTA	TGTCCTGATA	TTAGAGCCGT	GCAGTGCTAT	CCAGCCTCAC
501	TTCTCAGTCT	TTTTTGTGTT	TTGTTTTGTT	TTGTTTTGTT	TTGTTTTATT	TTTTTGAGAC	AGGGTTTCTC	TGTGAAGCCC	TGGGTGCTCT	GGAACCTACT
601	CTGTAGACCA	GGCTGGCCTC	GAACCTCAGAA	ATCCGCTGCG	CTCTGCCTCC	CGAGTGTCTG	GATTAAGAGC	GTGCGCCGCG	ACGCCCCGCG	TCACTTCTCA
701	GTCTTAGCTG	CTGTTACTTC	TCTGAGAAGC	ATCGAGGGCC	CTCACTAGTT	GATCCCTGGG	CTCGGGTCTG	CGTTTACTGT	GGGAGTCGGA	AGACTGGTTA
801	CCCGATTTTG	TACTGATACG	GAGATTTGCA	TTCTTGTTTA	CAGACCTCGG	CCACCGACCT	CGCAGACCAA	GCCGACCCGT	TGGTGACAGT	GAGCATATGC
901	TCTTCCCTGG	CCCGAAGTT	CCCGAAGCTG	ACCATCATAG	GGGAAGAGGT	GAGAGGCGCG	CGCCACTTGG	ATTCATACCC	TACCTGCCAT	TGAGCCGTAG
1001	GTTATGGTCA	GTCTTAGCGT	TGGCACTAAC	GTTCACACAC	AAAGCGATCG	TTTTCTTAG	GGGAAAAATC	TGACTTAATG	ATATTTTGGT	CCACTTAATG
1101	GGCTAAGTCT	CCATTTCTAG	TGATGGGAGC	TATGGTCACC	ATTGTAATAC	CATACGATGG	ACTCAGTGGC	AGAAAGTCGC	CTACTGTATG	TGAGGCTCTA
1201	AGGTGGGAGA	CATCTCAGTC	ATAAGACCAT	GTGGCTCACA	TATGCTAGTT	CTCGGCTGGG	AGCCCCGTGA	TCAGCAGTTA	TATGTGAAGA	GTCCGCAAGG
1301	TTCTGGAACT	CTGAGATGAC	TGGGCTTGGT	TGTGCTGTCT	GCTGTGCCGT	CATTTCAGAT	TGGACTGTGT	TACTTACAA	TGAACAATA	GACTATGTTT
1401	TAGTTTTGTT	TTTTATTAAG	TATGTTGTTT	GACAATTAG	TGCATACATG	TATACCATG	TGATTTCCCT	CATACCTCGG	ATTCCTCTCC	CCTCCCTTCC
1501	TTCTTGGCCC	GCCCCCTCTT	CCCCTTAGT	TTATTCAGGA	TCATCCATGT	GACCATTTCA	TTGGGACCAT	CCATTGGTCA	TCAGTGGTGC	ACAGGCTGAA
1601	GCAATGGCTT	CCCCCTTCCC	TGAATCAGTC	TGTAGGAAAT	AGTTTCTCAG	TGAAGGAGAG	AGAGTGTCTG	TCTGCATCTC	TCTCTCCACT	CTGCTTAACT
1701	GTGGGAGTAC	ATTCTTCTC	AGACCCAGCA	CAGTCATCTG	TTGTTGAGTA	TTGCCTGCTT	GCACCTGGCT	GCACCCAGT	AATGACGTTT	GGCAGGCTTT
1801	CTCCCCGTTT	TTACGCTCTT	ACCATCTTTC	TGCCCTCTCT	CTACAAGGCC	TGGTAAACCT	TAGAGGGGAT	AAATGTCTAA	ATATCTTATT	CAGAGCTGAG
1901	CAATCAGCTG	TAAGTTTGTG	TTATTAGGCC	TTCATATATC	TCTCCCTTCA	TTATAGTCTT	CTAGAAGAG	AATCTTCTCT	GACTAAGGCT	GAGTGGTAAT
2001	TCGCTATGTG	AAATAACATC	TATATTTAGG	AAGCTGTTTG	ACACTGTGTG	ACTTTAGTAA	AGCTGTAGAG	TTTAACCTCC	TAAGAGGACT	CATGGCCTCC
2101	CTTTTATATC	ACTGAGTGGG	TCTCCAGACA	TGGAGTGTGT	TTAACGTACT	AAGCGTGGAT	TCCCATGCTG	GAGTAGCCCT	CACATTCGAT	CAAGAGCAGG
2201	TAGTTACCCC	CCAAACAGTG	CGACACTGTT	GTTGTACGTC	TAGGCACAGC	TTGCCTGACA	GATGGTGTCT	TAGTTGTCTA	GGTGACAGA	TGGGCAATAC
2301	TTCTTCCCC	AGCAGCCTGC	AGAGAAAATG	TGTTACAGTC	TGACTTCTTT	GTCTCATGCA	ACCAAAGTGT	GTGGTGTCTA	TAGCAGTAAG	GTCTTAGCAT
2401	CTAATGCTAG	TGGGCAACCA	AGAAAAATGA	CAATGCCTAT	ATTGTCTTAG	GGCAGTGGGA	CCTCCGTGAC	CAACTTATCA	GGAGGCACCA	CACACACAGC
2501	AGGTGGGGTT	TTAATGAAGG	ATAATTTTCA	AGGGGAGCAG	TTTCTAGGTC	TCTCTCTTCC	AACCTAAAAA	AATGCATCCT	AGTTATTGTG	AGTAAATTTA
2601	AAATCAACAG	ATAAGTTAGT	TTCCAACAGT	CGCATGTGAG	GCCTCTGGAC	GTGTGGAAGA	CAGCAGTATT	CCATGTACTG	GAGTAGCTGG	CCATGTGCCG
2701	GAACAGCTGG	GCTACGGATG	CTGTTCTTAG	TGTTGTAAGG	AATTGCCACA	CCAGTTTCCA	TATGGCTGCA	CTGGTTTCCC	ACCAGCAATG	AAGGAGTCCC
2801	TCTTTTCCAC	CCTCACCAGC	ACTGCCTGTC	TTGAGGTTTC	TTACGGATTG	CCATTCTGAC	AGGACAAGAT	GAAATCTTAG	AGCAGCTTTA	ATTGTACTTT
2901	CTTTTGTGTC	TAATGATGTC	AAATACTTTT	TAAAATGTTT	ATTTTCAAT	CCATTACTTT	TTGAGAAATC	TCTGTTCACT	TCCATAGCCC	ATTTTGTCTG
3001	TTGTTTGTG	ACACAGGGTC	TTTCTCTATG	TATCCCTGGC	TATGCTGATG	AGAGTTACCT	CAAAGCTGAC	AGAGATCCAT	CTACTTTTAC	CTCCAGGTCG
3101	CTGGGATTAG	AGGCATGACG	ATTTTAAAG	TTATTAATAT	TTATTTGTGT	ACCTGTGTCT	GATCTGTGTA	TGTGGATGGA	TGTTTGTCTT	GCCTGGATAG
3201	CTCTGCTCCA	CATGTGAGCC	AGTTACCTCG	GGTGGCCAGA	AGAGGGCATC	GGATGCCCTG	GAACCTGGAG	TAGGATGGTT	GTGAGCTGCC	TGTGGGTGCT
3301	CGAACAACAG	CCTGGGTCTC	CGGGAGAGCA	GCCTGTGTTT	TACCTCCTAG	CCCACTCTCC	AGCTCCGGGG	GTGATTTCTT	TTCAAGAGA	CGAGAGAAGG
3401	CTGAGCTTTC	CCTCTTCTCC	GTGTAGACAT	CCAGTCTTCC	CAGCGCCAGT	TTGAGATGCT	CCCTCTCCCT	TCGTGATATT	TTGGTGTGTT	TTTCAAGAA
3501	CAGGTGGCTG	TAATGTATG	GCAATAGTCC	GGGTTTCCA	TCTGTTGCA	CTGATCTACA	CATCGGTTTT	TGTGCCAGCA	CCGTGCCCTT	TGTTACCTCG
3601	ATCTGTAGT	GTTATTTTGG	CTCAGAAATT	TTTTGGCTGC	CTGGGCTTTT	TGTGTTTTGC	ATCACTATT	CTACCGATCC	ATGAGCAGGG	AGACCTTTCA
3701	TCTACTAGTC	TCTGCCTTGA	TTTCTTTCTT	TAGAGTTTTT	TGAGCAGGGG	TCTCACATAT	AATCTTGGCT	GACCAGGAAC	TCAGTGTGTA	GACCAGGCTG
3801	GCCTCAAAC	CACAGAGTTC	TGCCTGCCTC	TGCCCTCTGA	TGCTGGGGT	TTAAGGCTTA	TGCCACTGGG	CCTGGGATTT	TCTCTGATTT	TAAAGTTTTT
3901	ATTGTAGAGG	TTCTTCACTT	CTTTGCTTGG	GTTCCTCTG	AGGTACTTTG	TTTATTAAAG	CTGCTATAAA	TGGGATTGTT	TTTCTGATTT	CTTCTTCAAC
4001	TTGTTTGCCA	TGGGATAAAA	AAAGCATGCC	ATGTGTGTAT	CCTGACAGAT	CAGAAGTGTT	AGTAATCTCA	GGAGCTTTCT	GGTGGAGACT	GTAGGCTCTC
4101	CCATGTACAG	CATTATATTC	TCTGTAGACA	GGAACACGCT	GTCTTCTTTA	TTTCTTACCT	ATATTCTTTT	CCCATCTTGT	TTTTATTGTT	TTAGCTAAGA
4201	CTAAACACCC	AAATCGATGG	CCCTGTCTCG	CTTCTAGTTT	TAATGTGTAT	GTTTGTTTGG	CAGGGTCTCG	TTACTTAGCC	CAGGCTGGCC	TTGAATCTT
4301	CCTGCTTCAT	CCAAACCACT	GCTGGGATTA	CCAGTACACA	GGAATCTATA	AAAAGGTTTT	TGTTTTTGTG	ATTGTTTTTA	TCTCTCTCTT	CTCTGCACT
4401	ACATTGCCCT	TCTGTGTGCT	GAGATCATGC	CAGAGTCTCG	TGTGTGCTGG	GCAATTAGTG	ACCACTGAGC	TGGATCCGAG	GTCCCTTGTG	TAACTCAATG
4501	CCAAGTTCT	TCCCATCTGC	AGCATTCCTC	AGCAATCCAA	AGCAAAATGG	GGAAACAGTA	ATATGTAAAG	GAAACTGGAT	GTATTTACAA	TTTTAGGTAA
4601	ACAGATATGA	GGAAAAGGTT	TTGGGTTTCT	TCTAGACGTT	CCTGAGTCAG	GGTTTACATG	TGGCTAGGAC	CCAGCCGTGA	GGCTTCTGTT	GAGGATGCTG
4701	TTCTCTGTG	TCATACTTCA	AACTAGGATG	GAAGCTCTGT	GGCCAACTCT	AGCTGTCTAC	TTCTCTCTTT	TGGGCTCTGT	CCAGTCTTAT	GCTAGGTTTG
4801	CTATAAAGC	TCTAAATATT	AGAGAAATTA	AACAGAAAGT	GCTAGGCGTG	CCATTGCT				4858

Fig 22B

	10	20	30	40	50	60	70	80	90	100
1	GTAGCACCTC	ACATACTCTC	CCAGCTCCAG	AGCTAGGCCC	CTCCTGGGGA	ATCACTGTTG	TACACTTCTT	TTCTTGAGGG	ACTGTGCTGA	CATGTCTGAC
101	TGGGCTAGAG	AAATGCTCCA	CCACCCCTGG	TCCCATAGCA	TCCCTCACC	TGAGGTTGTC	ACAGGTAAGA	AAACCAGAAG	GCATCGAATT	AAATCCAGAG
201	GTGTAAAAGT	CAGGAGGAGT	TGTGTGAGAG	CTCACACCTG	TAATCTCAGC	ACACTGGGGG	AGAGGGACTG	CTTTGAGTTT	GAGGCCATCT	TGAGTGCTAT
301	ACATGGCAAG	TTCTGGGTCA	GCTTGGGTTA	GAGCAAGACC	TTTTCTAGGC	AAAGCAAGAC	ATTAGTCAGA	AGAACCAGT	CTCAGAGCTG	GACTTCGGGT
401	TTTATTGTTT	TGTTTGTGTT	TTTTTATTTT	TTGAGACAGG	GTTTCTCTGT	GTAGCCCTGG	TTGTCTGTGC	ACTCACTTTG	TAGACCAGAC	TGGCCTCGAA
501	CTCAGAAATC	TGCTTGCCTC	TGCCTCCGGA	GTGCTGGGAT	TAAAGGTGTG	CGCCACCACT	GCTTGGCTTA	GACTTCAAGT	TTTAAAGGCC	TAGAGTTGTA
601	GTTTTGAAAT	AAAGATCTGC	ATTGAGAACT	TGTGAGGCTG	AGGCAGGAAG	ACTGTGAGGT	CAGCCTGGCC	TTCAAGTGA	GTTTCAGGTC	AGCCTGAGAT
701	AGAGGAGCAG	TGTGAGGCCA	GAAGGACCCC	ACAAAGAAAG	ACCTCCACAG	CGCTGCTTCT	AACGGGTCCA	GCTTCGAGAG	GCTTCTCAC	AGCTGCCAGA
801	GAGAATGTTG	TTGGCCCTCG	GAGGAGATAG	AGTGATAGTG	ACTCTGTGTG	TGTGTGTGTA	AATATATACT	GTATATACTG	TGAGGGTGCA	TGTGTGCAAC
901	ATGCATATGT	ACTGTGAAAA	TGTGTGAGAG	GCAGTGTGTT	CGTATGTGTG	TCTGTGAGTA	TAACCATATG	GTATGTAATC	T	981

Fig 23

# Triple-lox vectors for loxP/Cre targeted deletion

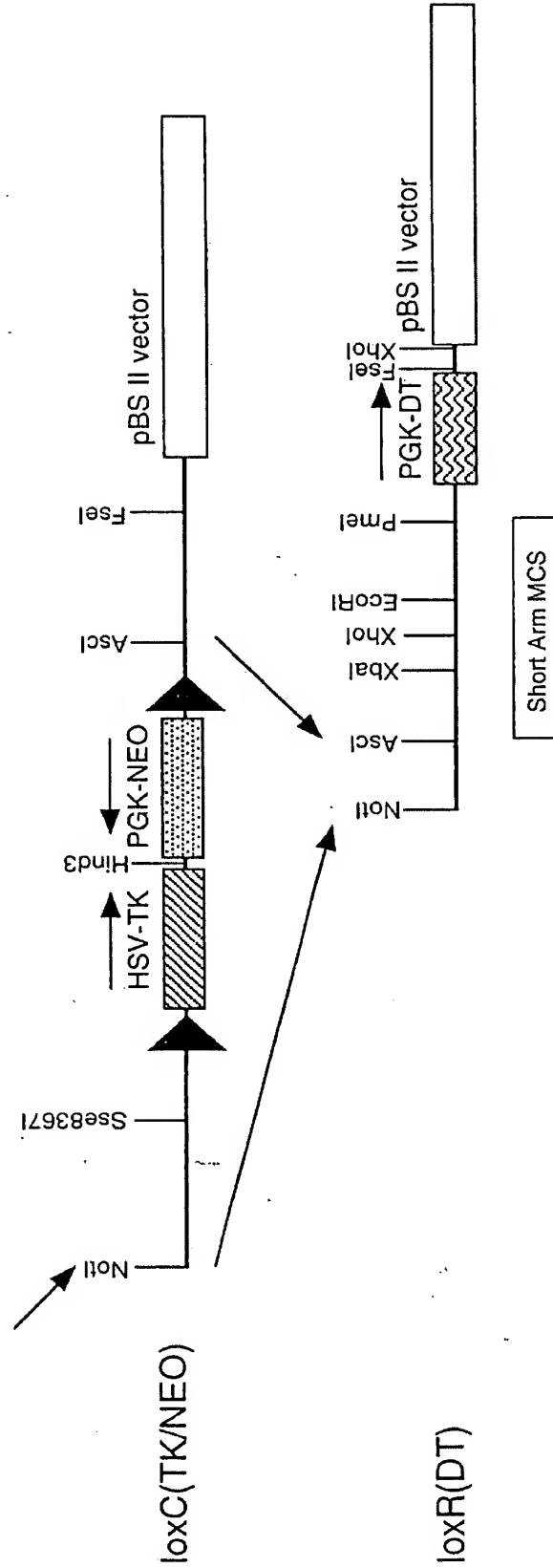


Fig 24

Structural motif involved in binding lithium

